AMENDMENT TO THE CLAIMS

Claim 1 (Withdrawn).   A computer-implemented method for making correct allele calls, comprising:

receiving data representing nucleic acid information;

applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

Claim 2 (Withdrawn).   The computer-implemented method of claim 1, wherein the allele calling algorithms applied in the step of applying at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 3 (Canceled).   A computer-implemented method for processing a signal, comprising:

receiving the signal representing nucleic acid information;

determining a complexity for the signal, the complexity relating to at least energy levels associated with the signal; and

making an allele call for the signal based on the determined complexity for the signal.

Claim 4 (Withdrawn). A computer-implemented method for making correct allele calls, comprising:

receiving signal representing nucleic acid information;

applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and

determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

Claim 5 (Withdrawn). The method of claim 4, wherein the applying step includes the substeps of:

creating a list of peaks in the signal;

determining characteristics associated with each peak; and

removing peaks from the list based on the determined characteristics.

Claim 6 (Canceled). The method of claim 3, wherein the signal is used to determine nucleic acid length, panel determination, and energy computation information.

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Claim 7 (Withdrawn). A computer-implemented method for interpreting nucleotide or amino acid information, comprising:

receiving data representing nucleotide or amino acid information;

applying at least two different algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

Claim 8 (Withdrawn).   The computer-implemented method of claim 7, wherein the algorithms applied in the step of applying at least two different algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 9 (Withdrawn).   A computer-implemented method for making correct allele calls associated with data representing nucleic acid information, comprising:

applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during

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application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

Claim 10 (Withdrawn). The computer-implemented method of claim 9, wherein the allele calling algorithms applied in the applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 11 (Withdrawn). A system for making correct allele calls, comprising:

a processor configured to execute program instructions; and

a memory containing program instructions for execution by the processor to

receive data representing nucleic acid information,

apply at least two different allele calling algorithms to the data to provide a result for each algorithm, and

depending on agreement between the results of each algorithm, identify an allele call within the data and assigning a confidence level for each call.

Claim 12 (Withdrawn).   The computer-implemented method of claim 11, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 13 (Withdrawn).   The system of claim 11, wherein the nucleic acid information comprises nucleic acid length.

Claim 14 (Canceled).   A system for processing a signal, comprising:

a processor configured to execute program instructions; and

a memory containing program instructions for execution by the processor to

receive the signal representing nucleic acid information,

determine a complexity for the signal, the complexity relating to at least energy levels associated with the signal, and

make an allele call for the signal based on the determined complexity for the signal.

Claim 15 (Canceled).   The system of claim 14, wherein the signal is used to determine nucleic acid length, panel determination, and energy computation information.

Claim 16 (Withdrawn).   A system for making correct allele calls, comprising:

a processor configured to execute program instructions; and

a memory containing program instructions for execution by the processor to

receive signal representing nucleic acid information,

apply a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker, and

determine that remaining peaks in the data are alleles after applying the set of filters to the signal.

Claim 17 (Withdrawn).   The system of claim 16, wherein when the processor executing program instructions applies the set of filters to the signal to eliminate peaks that do not represent alleles, the processor creates a list of peaks in the signal, determines characteristics associated with each peak, and removes peaks from the list based on the determined characteristics.

Claim 18 (Withdrawn).   The system of claim 16, wherein the nucleic acid information comprises nucleic acid length.

Claim 19 (Withdrawn).   A system for interpreting nucleotide or amino acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to

receive data representing nucleotide or amino acid information,

apply at least two different algorithms to the data to provide a result for each algorithm, and

depending on agreement between the results of each algorithm, identify at least one correct result within the data and assigning a confidence level to the at least one correct result.

Claim 20 (Withdrawn).   The system of claim 19, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 21 (Withdrawn).   A system for making correct allele calls associated with data representing nucleic acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to

apply   each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data,

if results from all of the applied allele calling algorithms are consistent, assign a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms,

if results from all of the applied allele calling algorithms are not consistent, assign   different levels of confidence for any allele calls identified in the data during

application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results, and

output a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

Claim 22 (Withdrawn).   The system of claim 21, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 23 (Withdrawn).   A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:

receiving data representing nucleic acid information;

applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

Claim 24 (Withdrawn).   The computer readable medium of claim 23, wherein the allele calling algorithms applied in the applying of at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 25 (Cancelled).   A computer-readable medium containing instructions for controlling a computer system to perform a method for processing a signal, the method comprising:

receiving the signal representing nucleic acid information;

determining a complexity for the signal, the complexity relating to at least energy levels associated with the signal; and

making an allele call for the signal based on the determined complexity for the signal.

Claim 26 (Withdrawn).   A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:

receiving signal representing nucleic acid information;

applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and

determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

Claim 27 (Withdrawn).   The computer readable medium of claim 26, wherein the applying of the set of filters includes:

creating a list of peaks in the signal;

determining characteristics associated with each peak; and

removing peaks from the list based on the determined characteristics.

Claim 28 (Canceled).   The method of claim 25, wherein the signal is used to determine nucleic acid length, panel determination, and energy computation information.

Claim 29 (Withdrawn).   A computer readable medium containing instructions for controlling a computer system to perform a method for interpreting nucleotide or amino acid information, the method comprising:

receiving data representing nucleotide or amino acid information;

applying at least two different algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

Claim 30 (Withdrawn).   The computer readable medium of claim 29, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 31(Withdrawn).   A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls associated with data representing nucleic acid information, the method comprising:

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applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

Claim 32 (Withdrawn).   The computer readable medium of claim 31, wherein the allele calling algorithms applied in the applying of each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

Claim 33 (Withdrawn).   A system for making correct allele calls, comprising:

means for receiving data representing nucleic acid information;

means for applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

means for depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

Claim 34 (New).   A computer-implemented method for processing a signal, comprising:

receiving the signal representing nucleic acid information;

analyzing the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and

making an allele call for the signal if the threshold test is met.

Claim 35 (New).   The method of claim 34, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy computation information.

Claim 36 (New).   The method of claim 35, wherein analyzing the signal includes:

determining if at least three panels exist in the signal; and

if at least three panels exist, computing an energy level for each panel.

Claim 37 (New).   The method of claim 36, wherein making an allele call includes:

comparing the computed energy levels of the panels to determine if the threshold test is met.

Claim 38 (New).   A system for processing a signal, comprising:

a memory containing program instructions; and

a processor configured to execute the program instructions in the memory and to:

receive the signal representing nucleic acid information;

analyze the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and

make an allele call for the signal if the threshold test is met.

Claim 39 (New).   The system of claim 38, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy computation information.

Claim 40 (New).   The system of claim 39, wherein the processor is further configured to determine if at least three panels exist in the signal, and if at least three panels exist, compute an energy level for each panel.

Claim 41 (New).   The system of claim 40, wherein the processor is further configured to compare the computed energy levels of the panels to determine if the threshold test is met.

Claim 42 (New).   A computer-readable medium containing instructions for controlling a computer system to perform a method for processing a signal, the method comprising:

receiving the signal representing nucleic acid information;

analyzing the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and

making an allele call for the signal if the threshold test is met.

Claim 43 (New).   The computer-readable medium of claim 42, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy computation information.

Claim 44 (New).   The computer-readable medium of claim 43, wherein the computer system is to further perform a method comprising:

determining if at least three panels exist in the signal; and

if at least three panels exist, computing an energy level for each panel.

Claim 45 (New).   The computer-readable medium of claim 44, wherein the computer system is to further perform a method comprising:

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comparing the computed energy levels of the panels to determine if the threshold test is met.